SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.
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    BAUGHN, Mariah R.

<120> HUMAN SCAD-RELATED MOLECULES, SCRM-1 AND SCRM-2

<130> PF-0559 USN

<140> 09/743,752
<141> Herewith

<150> PCT/US9916164
<151> 1999-07-16

<150> US 09/116,750
<151> 1998-07-16

<150> US 60/160,074
<151> 1998-07-16

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 278
<212> PRT
<213> HOMO SAPIENS

<220>
<221> misc_feature
<223> Incyte Clone No: 1240869

<400> 1
Met His Met Ala Arg Leu Leu Gly Leu Cys Ala Trp Ala Arg Lys Ser
1   5   10   15
Val Arg Met Ala Ser Ser Arg Met Thr Arg Arg Asp Pro Leu Thr Asn
            20   25   30
Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly Phe Ala Ile
            35   40   45
Ala Arg Arg Leu Ala Gln Asp Arg Ala His Val Val Val Ser Ser Arg
        50   55   60
Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr Leu Gln Gly Glu Gly
65   70   75   80
Leu Ser Val Thr Gly Thr Val Cys His Val Gly Lys Ala Glu Asp Arg
                85   90   95
Glu Arg Leu Val Ala Thr Ala Val Lys Leu His Gly Gly Ile Asp Ile
            100   105   110
Leu Val Ser Asn Ala Ala Val Asn Pro Phe Phe Gly Ser Ile Met Asp
            115   120   125

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Val Thr Glu Glu Val Trp Asp Lys Thr Leu Asp Ile Asn Val Lys Ala
    130             135             140
Pro Ala Leu Met Thr Lys Ala Val Val Pro Glu Met Glu Lys Arg Gly
145             150             155             160
Gly Gly Ser Val Val Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser
            165             170             175
Pro Gly Phe Ser Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu
            180             185             190
Asn Asn Thr Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn
        195             200             205
Cys Leu Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp
    210             215             220
Met Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
225             230             235             240
Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu Cys
            245             250             255
Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val Gly Gly
            260             265             270
Gly Thr Pro Ser Arg Leu
            275
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<210> 2
<211> 564
<212> PRT
<213> HOMO SAPIENS

<220>
<221> misc_feature
<223> Incyte Clone No: 2060002

<400> 2
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Met Ser Tyr Pro Ala Asp Asp Tyr Glu Ser Glu Ala Ala Tyr Asp Pro
  1             5              10             15
Tyr Ala Tyr Pro Ser Asp Tyr Asp Met His Thr Gly Asp Pro Lys Gln
            20             25             30
Asp Leu Ala Tyr Glu Arg Gln Tyr Glu Gln Gln Thr Tyr Gln Val Ile
            35             40             45
Pro Glu Val Ile Lys Asn Phe Ile Gln Tyr Phe His Lys Thr Val Ser
        50             55             60
Asp Leu Ile Asp Gln Lys Val Tyr Glu Leu Gln Ala Ser Arg Val Ser
65             70             75             80
Ser Asp Val Ile Asp Gln Lys Val Tyr Glu Ile Gln Asp Ile Tyr Glu
            85             90             95
Asn Ser Trp Thr Lys Leu Thr Glu Arg Phe Phe Lys Asn Thr Pro Trp
            100            105            110
Pro Glu Ala Glu Ala Ile Ala Pro Gln Val Gly Asn Asp Ala Val Phe
            115            120            125
Leu Ile Leu Tyr Lys Glu Leu Tyr Tyr Arg His Ile Tyr Ala Lys Val
        130            135            140
Ser Gly Gly Pro Ser Leu Glu Gln Arg Phe Glu Ser Tyr Tyr Asn Tyr
145            150            155            160
Cys Asn Leu Phe Asn Tyr Ile Leu Asn Ala Asp Gly Pro Ala Pro Leu
            165            170            175
Glu Leu Pro Asn Gln Trp Leu Trp Asp Ile Ile Asp Glu Phe Ile Tyr
            180            185            190
Gln Phe Gln Ser Phe Ser Gln Tyr Arg Cys Lys Thr Ala Lys Lys Ser
            195            200            205
```

```
Glu Glu Glu Ile Asp Phe Leu Arg Ser Asn Pro Lys Ile Trp Asn Val
210                 215                 220
His Ser Val Leu Asn Val Leu His Ser Leu Val Asp Lys Ser Asn Ile
225                 230                 235                 240
Asn Arg Gln Leu Glu Val Tyr Thr Ser Gly Gly Asp Pro Glu Ser Val
                245                 250                 255
Ala Gly Glu Tyr Gly Arg His Ser Leu Tyr Lys Met Leu Gly Tyr Phe
                260                 265                 270
Ser Leu Val Gly Leu Leu Arg Leu His Ser Leu Leu Gly Asp Tyr Tyr
                275                 280                 285
Gln Ala Ile Lys Val Leu Glu Asn Ile Glu Leu Asn Lys Lys Ser Met
290                 295                 300
Tyr Ser Arg Val Pro Glu Cys Gln Val Thr Thr Tyr Tyr Tyr Val Gly
305                 310                 315                 320
Phe Ala Tyr Leu Met Met Arg Arg Tyr Gln Asp Ala Ile Arg Val Phe
                325                 330                 335
Ala Asn Ile Leu Leu Tyr Ile Gln Arg Thr Lys Ser Met Phe Gln Arg
                340                 345                 350
Thr Thr Tyr Lys Tyr Glu Met Ile Asn Lys Gln Asn Glu Gln Met His
                355                 360                 365
Ala Leu Leu Ala Ile Ala Leu Thr Met Tyr Pro Met Arg Ile Asp Glu
370                 375                 380
Ser Ile His Leu Gln Leu Arg Glu Lys Tyr Gly Asp Lys Met Leu Arg
385                 390                 395                 400
Met Gln Lys Gly Asp Pro Gln Val Tyr Glu Glu Leu Phe Ser Tyr Ser
                405                 410                 415
Cys Pro Lys Phe Leu Ser Pro Val Val Pro Asn Tyr Asp Asn Val His
                420                 425                 430
Pro Asn Tyr His Lys Glu Pro Phe Leu Gln Gln Leu Lys Val Phe Ser
                435                 440                 445
Asp Glu Val Gln Gln Gln Ala Gln Leu Ser Thr Ile Arg Ser Phe Leu
450                 455                 460
Lys Leu Tyr Thr Thr Met Pro Val Ala Lys Leu Ala Gly Phe Leu Asp
465                 470                 475                 480
Leu Thr Glu Gln Glu Phe Arg Ile Gln Leu Leu Val Phe Lys His Lys
                485                 490                 495
Met Lys Asn Leu Val Trp Thr Ser Gly Ile Ser Ala Leu Asp Gly Glu
                500                 505                 510
Phe Gln Ser Ala Ser Glu Val Asp Phe Tyr Ile Asp Lys Asp Met Ile
                515                 520                 525
His Ile Ala Asp Thr Lys Val Ala Arg Arg Tyr Gly Asp Phe Phe Ile
530                 535                 540
Arg Gln Ile His Lys Phe Glu Glu Leu Asn Arg Thr Leu Lys Lys Met
545                 550                 555                 560
Gly Gln Arg Pro
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<210> 3
<211> 1280
<212> DNA
<213> HOMO SAPIENS

<220>
<221> misc_feature
<223> Incyte Clone No: 1240869

<400> 3

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gagtggaacc cagacttgct ggtctgatcc atgcacatgg ccaggctgct aggcctctgt    60
gcctgggcac ggaagtcggt gcggatggcc agctccagga tgacccgccg ggacccgctc   120
acaaataagg tggccctggt aacggcctcc accgacggga tcggcttcgc catcgcccgg   180
cgtttggccc aggacagggc ccacgtggtc gtcagcagcc ggaagcagca gaatgtggac   240
caggcggtgg ccacgctgca gggggagggg ctgagcgtga cgggcaccgt gtgccatgtg   300
gggaaggcgg aggaccggga gcggctggtg gccacggctg tgaagcttca tggaggtatc   360
gatatcctag tctccaatgc tgctgtcaac cctttctttg gaagcataat ggatgtcact   420
gaggaggtgt gggacaagac tctggacatt aatgtgaagg ccccagccct gatgacaaag   480
gcagtggtgc cagaaatgga gaaacgagga ggcggctcag tggtgatcgt gtcttccata   540
gcagccttca gtccatctcc tggcttcagt ccttacaatg tcagtaaaac agccttgctg   600
ggcctcaaca atacccctggc catagagctg gccccaagga acattagggt gaactgccta   660
gcacctggac ttatcaagac tagcttcagc aggatgctct ggatggacaa ggaaaaagag   720
gaaagcatga aagaaaccct gcggataaga aggttaggcg agccagagga ttgtgctggc   780
atcgtgtctt tcctgtgctc tgaagatgcc agctacatca ctggggaaac agtggtggtg   840
ggtggaggaa ccccgtcccg cctctgagga ccgggagaca gcccacaggc cagagttggg   900
ctctagctcc tggtgctgtt cctgcattca cccactggcc tttcccacct ctgctcacct   960
tactgttcac ctcatcaaat cagttctgcc ctgtgaaaag atccagcctt ccctgccgtc  1020
aaggtggcgt cttactcggg attcctgctg ttgttgtggc cttgggtaaa ggcctcccct  1080
gagaacacag gacaggcctg ctgacaaggc tgagtctacc ttggcaaaga ccaagatatt  1140
ttttcctggg ccactgggga atctgagggg tgatgggaga gaaggaacct ggagtggaag  1200
gagcagagtt gcaaattaac aacttgcaaa tgaggtgcaa ataaaatgca gatgattgcg  1260
cggctttgaa aaaaaaaaaa                                             1280
```

<210> 4
<211> 1894
<212> DNA
<213> HOMO SAPIENS

<220>
<221> misc_feature
<223> Incyte Clone No: 2060002

<400> 4

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ctcgcaagcg aggcagccat gtcttatccc gctgatgatt atgagtctga ggcggcttat    60
gacccctacg cttatcccag cgactatgat atgcacacag gagatccaaa gcaggacctt   120
gcttatgaac gtcagtatga acagcaaacc tatcaggtga ccctgaggt gatcaaaaac   180
ttcatccagt atttccacaa aactgtctca gatttgattg accagaaagt gtatgagcta   240
caggccagtc gtgtctccag tgatgtcatt gaccagaagg tgtatgagat ccaggacatc   300
tatgagaaca gctggaccaa gctgactgaa agattcttca agaatacacc ttggccgag   360
gctgaagcca ttgctccaca ggttggcaat gatgctgtct tcctgatttt atacaaagaa   420
ttatactaca ggcacatata tgccaaagtc agtgggggac cttccttgga gcagaggttt   480
gaatcctatt acaactactg caatctcttc aactacattc ttaatgccga tggtcctgct   540
ccccttgaac tacccaacca gtggctctgg gatattatcg atgagttcat ctaccagttt   600
cagtcattca gtcagtaccg ctgtaagact gccaagaagt cagaggagga gattgacttt   660
cttcgttcca atcccaaaat ctggaatgtt catagtgtcc tcaatgtcct tcattccctg   720
gtagacaaat ccaacatcaa ccgacagttg gaggtataca caagcggagg tgaccctgag   780
agtgtggctg gggagtatgg gcggcactcc ctctacaaaa tgcttggtta cttcagcctg   840
gtcgggcttc tccgcctgca ctccctgtta ggagattact accaggccat caaggtgctg   900
gagaacatcg aactgaacaa gaagagtatg tattcccgtg tgccagagtg ccaggtcacc   960
acatactatt atgttgggtt tgcatatttg atgatgcgtc gttaccagga tgccatccgg  1020
gtcttcgcca acatcctcct ctacatccag aggaccaaga gcatgttcca gaggaccacg  1080
tacaagtatg agatgattaa caagcagaat gagcagatgc atgcgctgct ggccattgcc  1140
ctcacgatgt accccatgcg tatcgatgag agcattcacc tccagctgcg ggagaaatat  1200
ggggacaaga tgttgcgcat gcagaaaggt gacccacaag tctatgaaga acttttcagt  1260
tactcctgcc ccaagttcct gtcgcctgta gtgcccaact atgataatgt gcaccccaac  1320
taccacaaag agcccttcct gcagcagctg aaggtgtttt ctgatgaagt acagcagcag  1380
```

```
gcccagcttt caaccatccg cagcttcctg aagctctaca ccaccatgcc tgtggccaag    1440
ctggctggct tcctggacct cacagagcag gagttccgga tccagcttct tgtcttcaaa    1500
cacaagatga agaacctcgt gtggaccagc ggtatctcag ccctggatgg tgaatttcag    1560
tcagcctcag aggttgactt ctacattgat aaggacatga tccacatcgc ggacaccaag    1620
gtcgccaggc gttatgggga tttcttcatc cgtcagatcc acaaatttga ggagcttaat    1680
cgaaccctga agaagatggg acagagacct tgatgatatt cacacacatt caggaacctg    1740
ttttgatgta ttataggcag gaagtgtttt tgctaccgtg aaaccttac ctagatcagc     1800
catcagcctg tcaactcagt taacaagtta aggaccgaag tgtttcaagt ggatctcagt    1860
aaaggatctt tggagccaga aaaaaaaaaa aaaa                                 1894
```

<210> 5
<211> 280
<212> PRT
<213> HOMO SAPIENS

<220>
<221> misc_feature
<223> GENBANK ID: g1079566

<400> 5

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1               5                   10                  15
Ala Arg Leu Ser Val Arg Met Ser Ser Thr Gly Ile Asp Arg Lys Gly
            20                  25                  30
Val Leu Ala Asn Arg Val Ala Val Thr Gly Ser Thr Ser Gly Ile
            35                  40                  45
Gly Phe Ala Ile Ala Arg Arg Leu Ala Arg Asp Gly Ala His Val Val
        50                  55                  60
Ile Ser Ser Arg Lys Gln Gln Asn Val Asp Arg Ala Met Ala Lys Leu
65                  70                  75                  80
Gln Gly Glu Gly Leu Ser Val Ala Gly Ile Val Cys His Val Gly Lys
                85                  90                  95
Ala Glu Asp Arg Glu Gln Leu Val Ala Lys Ala Leu Glu His Cys Gly
            100                 105                 110
Gly Val Asp Phe Leu Val Cys Ser Ala Gly Val Asn Pro Leu Val Gly
            115                 120                 125
Ser Thr Leu Gly Thr Ser Glu Gln Ile Trp Asp Lys Ile Leu Ser Val
            130                 135                 140
Asn Val Lys Ser Pro Ala Leu Leu Leu Ser Gln Leu Leu Pro Tyr Met
145                 150                 155                 160
Glu Asn Arg Arg Gly Ala Val Ile Leu Val Ser Ser Ile Ala Ala Tyr
                165                 170                 175
Asn Pro Val Val Ala Leu Gly Val Tyr Asn Val Ser Lys Thr Ala Leu
            180                 185                 190
Leu Gly Leu Thr Arg Thr Leu Ala Leu Glu Leu Ala Pro Lys Asp Ile
            195                 200                 205
Arg Val Asn Cys Val Val Pro Gly Ile Ile Lys Thr Asp Phe Ser Lys
            210                 215                 220
Val Phe His Gly Asn Glu Ser Leu Trp Lys Asn Phe Lys Glu His His
225                 230                 235                 240
Gln Leu Gln Arg Ile Gly Glu Ser Glu Asp Cys Ala Gly Ile Val Ser
                245                 250                 255
Phe Leu Cys Ser Pro Asp Ala Ser Tyr Val Asn Gly Glu Asn Ile Ala
            260                 265                 270
Val Ala Gly Tyr Ser Thr Arg Leu
            275                 280
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<210> 6
<211> 938
<212> PRT
<213> CAENORHABDITIS ELEGANS

<220>
<221> misc_feature
<223> GENBANK ID: g2731377

<400> 6

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 1               5                  10                  15
Arg Arg Arg Thr Asn Thr Phe Ser Ser Asp Glu Asp Gly Val Pro Asn
            20                  25                  30
Glu Val Ala Asp Tyr Leu Val Tyr Phe Ser Arg Met Val Asp Glu Gln
            35                  40                  45
Asn Val Pro Glu Ile Leu Thr Leu Tyr Asp Gln Ala Phe Pro Asp Leu
        50                  55                  60
Thr Glu Arg Phe Phe Arg Asp Arg Met Trp Pro Asp Glu Asn Val Val
65                  70                  75                  80
Glu Arg Ile Ile Gly Pro Gly Asn Lys Leu Phe Ile Ile Leu Tyr Lys
                85                  90                  95
Glu Leu Tyr Tyr Arg Gln Leu Tyr Ala Arg Asn Thr Arg Gly Pro Leu
            100                 105                 110
Leu Val His Arg Tyr Glu Ser Phe Met Asn Tyr Gln Glu Leu Phe Ser
            115                 120                 125
Glu Leu Leu Ser Ser Lys Asp Pro Ile Pro Leu Ser Leu Pro Asn Val
        130                 135                 140
Trp Leu Trp Asp Ile Ile Asp Glu Phe Val Tyr Gln Phe Gln Ala Phe
145                 150                 155                 160
Cys Leu Tyr Lys Ala Asn Pro Gly Lys Arg Asn Ala Asp Glu Val Glu
                165                 170                 175
Asp Leu Ile Asn Ile Glu Glu Asn Gln Asn Ala Trp Asn Ile Tyr Pro
                180                 185                 190
Val Leu Asn Ile Leu Tyr Ser Leu Leu Ser Lys Ser Gln Ile Val Glu
            195                 200                 205
Gln Leu Lys Ala Leu Lys Glu Lys Arg Asn Pro Asp Ser Val Ala Asp
        210                 215                 220
Glu Phe Gly Gln Ser Asp Leu Tyr Phe Lys Leu Gly Tyr Phe Ala Leu
225                 230                 235                 240
Ile Gly Leu Leu Arg Thr His Val Leu Leu Gly Asp Tyr His Gln Ala
                245                 250                 255
Leu Lys Thr Val Gln Tyr Val Asp Ile Asp Pro Lys Gly Ile Tyr Asn
            260                 265                 270
Thr Val Pro Thr Cys Leu Val Thr Leu His Tyr Phe Val Gly Phe Ser
            275                 280                 285
His Leu Met Met Arg Asn Tyr Gly Glu Ala Thr Lys Met Phe Val Asn
        290                 295                 300
Cys Leu Leu Tyr Ile Gln Arg Thr Lys Ser Val Gln Asn Gln Gln Pro
305                 310                 315                 320
Ser Lys Lys Asn Phe Gln Tyr Asp Val Ile Gly Lys Thr Trp Asp Gln
                325         .       330                 335
Leu Phe His Leu Leu Ala Ile Cys Leu Ala Ile Gln Pro Gln Arg Ile
            340                 345                 350
Asp Glu Ser Ile Ala Ser Gln Leu Ser Glu Arg Cys Gly Glu Arg Met
            355                 360                 365
Met His Met Ala Asn Gly Asn Ile Asp Glu Phe Arg Asn Ala Phe Ala
```

```
              370                      375                      380
Thr Gly Cys Pro Lys Phe Leu Ser Pro Thr Thr Val Val Tyr Glu Gly
385                      390                      395                      400
Val Asn Gln Ser Lys Glu Pro Leu Leu Arg Gln Thr Gln Ser Phe Leu
                        405                      410                      415
Glu Gly Ile Glu Ser Gln Met Ala Leu Pro Val Leu Arg Gly Tyr Leu
                        420                      425                      430
Lys Leu Tyr Thr Thr Leu Pro Thr Lys Lys Leu Ala Ser Phe Met Asp
                        435                      440                      445
Val Asp Asp Glu His Tyr Asp Ser Phe Ile Gly Lys Leu Leu Thr Tyr
                        450                      455                      460
Lys Met Ile Val Asn Glu Leu Gly Lys Glu Ala Gly Pro Ser Ser Ala
465                      470                      475                      480
Asp Asp Asp Glu Pro Gln Thr Asp Ile Asp Phe Tyr Val Asp Arg Asp
                        485                      490                      495
Met Ile Asn Ile Ala Asp Thr Lys Val Ala Arg His Val Gly Cys Ala
                        500                      505                      510
Gln Thr Thr Arg Tyr Pro Glu Thr Met Ile Leu Lys Lys Lys Phe Val
                        515                      520                      525
Gly Arg Thr Val Leu Ile Thr Gly Ala Ser Arg Gly Ile Gly Lys Glu
                        530                      535                      540
Ile Ala Leu Lys Leu Ala Lys Asp Gly Ala Asn Ile Val Val Ala Ala
545                      550                      555                      560
Lys Thr Ala Thr Ala His Pro Lys Leu Pro Gly Thr Ile Tyr Ser Ala
                        565                      570                      575
Ala Glu Glu Ile Glu Lys Ala Gly Gly Lys Ala Leu Pro Cys Ile Val
                        580                      585                      590
Asp Val Arg Asp Glu Ala Ser Val Lys Ala Ser Val Glu Glu Ala Val
                        595                      600                      .605   .
Lys Lys Phe Gly Gly Ile Asp Ile Leu Ile Asn Asn Ala Ser Ala Ile
                        610                      615                      620
Ser Leu Thr Asp Thr Glu Asn Thr Glu Met Lys Arg Tyr Asp Leu Met
625                      630                      635                      640
His Ser Ile Asn Thr Arg Gly Thr Phe Leu Met Thr Lys Thr Cys Leu
                        645                      650                      655
Pro Tyr Leu Lys Ser Gly Lys Asn Pro His Val Leu Asn Ile Ser Pro
                        660                      665                      670
Pro Leu Leu Met Glu Thr Arg Trp Phe Ala Asn His Val Ala Tyr Thr
                        675                      680                      685
Met Ala Lys Tyr Gly Met Ser Met Cys Val Leu Gly Gln His Glu Glu
                        690                      695                      700
Phe Arg Pro His Gly Ile Ala Val Asn Ala Leu Trp Pro Leu Thr Ala
705                      710                      715                      720
Ile Trp Thr Ala Ala Met Glu Met Leu Ser Asp Lys Gly Gly Glu Ala
                        725                      730                      735
Gly Ser Arg Lys Pro Ser Ile Met Ala Asp Ala Ala Tyr Ala Val Leu
                        740                      745                      750
Ser Lys Asn Ser Lys Asp Phe Thr Gly Asn Phe Cys Ile Asp Glu Asp
                        755                      760                      765
Ile Leu Lys Ala Glu Gly Val Thr Asp Phe Asp Arg Tyr Ala Cys Val
                        770                      775                      780
Pro Asp Ala Pro Leu Met Pro Asp Phe Phe Ile Pro Ala Gly Thr Tyr
785                      790                      795                      800
Asp His Lys Phe Ser Ser Gly Ala Gln Ile Gly Lys Lys Asn Lys Thr
                        805                      810                      815
His Glu Ala Gly Val Val Glu Glu Glu Ile Lys Gln Ile Phe Thr Ser
                        820                      825                      830
```

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```
Ala Lys Arg Leu Leu Asn Ala Asp Ile Val Lys Lys Thr Gly Phe Val
        835                 840             845
Tyr Glu Phe Leu Leu Lys Asp Pro Thr Thr Lys Ser Glu Arg Ile Ile
    850                 855             860
Thr Leu Asp Leu Lys Asn Gly Glu Gly Ala Leu Thr Asp Lys Lys Ala
865                 870             875                 880
Ser Gly Lys Ala Asp Val Lys Phe Thr Leu Ala Pro Glu His Phe Ala
                885             890             895
Pro Leu Phe Thr Gly Lys Leu Arg Pro Thr Thr Ala Leu Met Thr Lys
            900             905             910
Lys Leu Gln Ile Ser Gly Asp Met Pro Gly Ala Met Lys Leu Glu Ser
        915             920             925
Leu Leu Arg Lys Phe Thr Glu Gly Lys Leu
    930             935
```